

=> d his full

(FILE 'HOME' ENTERED AT 17:33:10 ON 11 APR 2007)

INDEX 'ADISCTI, ADISINSIGHT, ADISNEWS, AGRICOLA, ANABSTR, ANTE, AQUALINE,
AQUASCI, BIOENG, BIOSIS, BIOTECHABS, BIOTECHDS, BIOTECHNO, CABA, CAPLUS,
CEABA-VTB, CIN, CONFSCI, CROPB, CROPU, DDFB, DDFU, DGENE, DISSABS, DRUGB,
DRUGMONOG2, DRUGU, EMBAL, EMBASE, ...' ENTERED AT 17:33:40 ON 11 APR 2007
SEA RESTRICTI? (S) (ENZYM? OR ENDONUCLEAS?)

31 FILE ADISCTI
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84 FILE PHIN
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19895 FILE SCISEARCH
9853 FILE TOXCENTER
65679 FILE USPATFULL
7383 FILE USPAT2
1 FILE VETB
161 FILE VETU
68 FILE WATER
8559 FILE WPIDS

31 FILE WPIFV
8559 FILE WPINDEX
42 FILE IPA
4 FILE NAPRALERT
555 FILE NLDB

L1 QUE RESTRICTI? (S) (ENZYM? OR ENDONUCLEAS?)

D RANK

FILE 'GENBANK, USPATFULL, MEDLINE, CAPLUS, BIOSIS, EMBASE, SCISEARCH,
BIOTECHNO, LIFESCI, PASCAL, CABA' ENTERED AT 17:37:30 ON 11 APR 2007

L2 790629 SEA RESTRICTI? (S) (ENZYM? OR ENDONUCLEAS?)

L3 739 SEA L2(S) PYLORI?

L4 49 SEA L3 AND (BCC? OR ?CCATC?)

L5 47 DUP REM L4 (2 DUPLICATES REMOVED)

D TI L5 1-45

D TI L5 46-47

L6 31 SEA L3 AND (BCC? OR CCATC?)

L7 29 DUP REM L6 (2 DUPLICATES REMOVED)

D L7 1-29

Connecting via Winsock to STN

Welcome to STN International! Enter x:x

LOGINID:ssspta1652dmr

PASSWORD:

TERMINAL (ENTER 1, 2, 3, OR ?):2

* * * * * Welcome to STN International * * * * *

NEWS 1 Web Page URLs for STN Seminar Schedule - N. America
NEWS 2 "Ask CAS" for self-help around the clock
NEWS 3 DEC 18 CA/CAPLUS pre-1967 chemical substance index entries enhanced
with preparation role
NEWS 4 DEC 18 CA/CAPLUS patent kind codes updated
NEWS 5 DEC 18 MARPAT to CA/CAPLUS accession number crossover limit increased
to 50,000
NEWS 6 DEC 18 MEDLINE updated in preparation for 2007 reload
NEWS 7 DEC 27 CA/CAPLUS enhanced with more pre-1907 records
NEWS 8 JAN 08 CHEMLIST enhanced with New Zealand Inventory of Chemicals
NEWS 9 JAN 16 CA/CAPLUS Company Name Thesaurus enhanced and reloaded
NEWS 10 JAN 16 IPC version 2007.01 thesaurus available on STN
NEWS 11 JAN 16 WPIDS/WPINDEX/WPIX enhanced with IPC 8 reclassification data
NEWS 12 JAN 22 CA/CAPLUS updated with revised CAS roles
NEWS 13 JAN 22 CA/CAPLUS enhanced with patent applications from India
NEWS 14 JAN 29 PHAR reloaded with new search and display fields
NEWS 15 JAN 29 CAS Registry Number crossover limit increased to 300,000 in
multiple databases
NEWS 16 FEB 15 PATDPASPC enhanced with Drug Approval numbers
NEWS 17 FEB 15 RUSSIAPAT enhanced with pre-1994 records
NEWS 18 FEB 23 KOREAPAT enhanced with IPC 8 features and functionality
NEWS 19 FEB 26 MEDLINE reloaded with enhancements
NEWS 20 FEB 26 EMBASE enhanced with Clinical Trial Number field
NEWS 21 FEB 26 TOXCENTER enhanced with reloaded MEDLINE
NEWS 22 FEB 26 IFICDB/IFIPAT/IFIUDB reloaded with enhancements
NEWS 23 FEB 26 CAS Registry Number crossover limit increased from 10,000
to 300,000 in multiple databases
NEWS 24 MAR 15 WPIDS/WPIX enhanced with new FRAGHITSTR display format
NEWS 25 MAR 16 CASREACT coverage extended
NEWS 26 MAR 20 MARPAT now updated daily
NEWS 27 MAR 22 LWPI reloaded
NEWS 28 MAR 30 RDISCLOSURE reloaded with enhancements
NEWS 29 MAR 30 INPADOCDB will replace INPADOC on STN
NEWS 30 APR 02 JICST-EPLUS removed from database clusters and STN

NEWS EXPRESS NOVEMBER 10 CURRENT WINDOWS VERSION IS V8.01c, CURRENT
MACINTOSH VERSION IS V6.0c(ENG) AND V6.0Jc(JP),
AND CURRENT DISCOVER FILE IS DATED 25 SEPTEMBER 2006.

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NEWS IPC8 For general information regarding STN implementation of IPC 8
NEWS X25 X.25 communication option no longer available

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* * * * * STN Columbus * * * * *

FILE 'HOME' ENTERED AT 17:33:10 ON 11 APR 2007

=> index bioscience medicine

FILE 'DRUGMONOG' ACCESS NOT AUTHORIZED

COST IN U.S. DOLLARS

SINCE FILE

ENTRY TOTAL

SESSION

FULL ESTIMATED COST

0.21

0.21

INDEX 'ADISCTI, ADISINSIGHT, ADISNEWS, AGRICOLA, ANABSTR, ANTE, AQUALINE, AQUASCI, BIOENG, BIOSIS, BIOTECHABS, BIOTECHDS, BIOTECHNO, CABA, CAPLUS, CEABA-VTB, CIN, CONFSCI, CROPB, CROPU, DDFB, DDFU, DGENE, DISSABS, DRUGB, DRUGMONOG2, DRUGU, EMBAL, EMBASE, ...' ENTERED AT 17:33:40 ON 11 APR 2007

70 FILES IN THE FILE LIST IN STNINDEX

Enter SET DETAIL ON to see search term postings or to view search error messages that display as 0* with SET DETAIL OFF.

=>

=> s restricti? (s) (enzym? or endonucleas?)

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27 FILE ADISNEWS
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16 FILE ANTE
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10704 FILE CABA
37645 FILE CAPLUS
790 FILE CEABA-VTB
81 FILE CIN
319 FILE CONFSCI
4 FILE CROPB
133 FILE CROPU
29 FILE DDFB

21 FILES SEARCHED...

170 FILE DDFU
38469 FILE DGENE
2384 FILE DISSABS
29 FILE DRUGB
566 FILE DRUGU
125 FILE EMBAL
21269 FILE EMBASE
10560 FILE ESBIODBASE
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411 FILE FROSTI
1211 FILE FSTA
515097 FILE GENBANK
61 FILE HEALSAFE
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9 FILE IMSRESEARCH
25 FILE KOSMET

17980 FILE LIFESCI
 42 FILES SEARCHED...
 39232 FILE MEDLINE
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 371 FILE OCEAN
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 65679 FILE USPATFULL
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 161 FILE VETU
 68 FILE WATER
 8559 FILE WPIDS
 65 FILES SEARCHED...
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 42 FILE IPA
 4 FILE NAPRALERT
 555 FILE NLDB

63 FILES HAVE ONE OR MORE ANSWERS, 70 FILES SEARCHED IN STNINDEX

L1 QUE RESTRICTI? (S) (ENZYM? OR ENDONUCLEAS?)

=> d rank

| | | |
|-----|--------|------------|
| F1 | 515097 | GENBANK |
| F2 | 65679 | USPATFULL |
| F3 | 39232 | MEDLINE |
| F4 | 38469 | DGENE |
| F5 | 37645 | CAPLUS |
| F6 | 30282 | BIOSIS |
| F7 | 21269 | EMBASE |
| F8 | 19895 | SCISEARCH |
| F9 | 19601 | BIOTECHNO |
| F10 | 17980 | LIFESCI |
| F11 | 13245 | PASCAL |
| F12 | 10704 | CABA |
| F13 | 10641 | BIOTECHABS |
| F14 | 10641 | BIOTECHDS |
| F15 | 10560 | ESBIOBASE |
| F16 | 9853 | TOXCENTER |
| F17 | 8559 | WPIDS |
| F18 | 8559 | WPINDEX |
| F19 | 7383 | USPAT2 |
| F20 | 6488 | IFIPAT |
| F21 | 3911 | AGRICOLA |
| F22 | 3267 | BIOENG |
| F23 | 2384 | DISSABS |
| F24 | 1216 | AQUASCI |
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| F26 | 790 | CEABA-VTB |
| F27 | 745 | PROMT |
| F28 | 566 | DRUGU |
| F29 | 555 | NLDB |
| F30 | 411 | FROSTI |
| F31 | 371 | OCEAN |
| F32 | 319 | CONFSCI |

| | | |
|-----|-----|-------------|
| F33 | 240 | NTIS |
| F34 | 170 | DDFU |
| F35 | 161 | VETU |
| F36 | 133 | CROPU |
| F37 | 125 | EMBAL |
| F38 | 116 | ANABSTR |
| F39 | 84 | PHIN |
| F40 | 81 | CIN |
| F41 | 68 | WATER |
| F42 | 61 | HEALSAFE |
| F43 | 42 | IPA |
| F44 | 41 | AQUALINE |
| F45 | 31 | ADISCTI |
| F46 | 31 | WPIFV |
| F47 | 29 | DDFB |
| F48 | 29 | DRUGB |
| F49 | 27 | ADISNEWS |
| F50 | 25 | KOSMET |
| F51 | 16 | ANTE |
| F52 | 16 | FOREGE |
| F53 | 12 | IMSDRUGNEWS |
| F54 | 10 | ADISINSIGHT |
| F55 | 9 | IMSRESEARCH |
| F56 | 6 | PHARMAML |
| F57 | 4 | CROPB |
| F58 | 4 | NAPRALERT |
| F59 | 3 | PROUSDDR |
| F60 | 3 | RDISCLOSURE |
| F61 | 1 | NUTRACEUT |
| F62 | 1 | PHAR |
| F63 | 1 | VETB |

=> file f1-f3, f5-12

COST IN U.S. DOLLARS

SINCE FILE

ENTRY

TOTAL

SESSION

FULL ESTIMATED COST

3.78

3.99

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FILE 'USPATFULL' ENTERED AT 17:37:30 ON 11 APR 2007

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FILE 'MEDLINE' ENTERED AT 17:37:30 ON 11 APR 2007

FILE 'CAPLUS' ENTERED AT 17:37:30 ON 11 APR 2007

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FILE 'LIFESCI' ENTERED AT 17:37:30 ON 11 APR 2007

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FILE 'CABA' ENTERED AT 17:37:30 ON 11 APR 2007
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=> s restricti? (s) (enzym? or endonucleas?)
L2 790629 RESTRICTI? (S) (ENZYM? OR ENDONUCLEAS?)

=> s l2(s) pylori?
L3 739 L2(S) PYLORI?

=> s l3 and (bcc? or ?ccatc?)
2 FILES SEARCHED...

LEFT TRUNCATION IGNORED FOR FILE 'LIFESCI'

L4 49 L3 AND (BCC? OR ?CCATC?)

Left truncation is not valid in the specified search field in the
specified file. The term has been searched without left truncation.
Examples: '?TERPEN?' would be searched as 'TERPEN?' and '?FLAVONOID'
would be searched as 'FLAVONOID.'

If you are searching in a field that uses implied proximity, and you
used a truncation symbol after a punctuation mark, the system may
interpret the truncation symbol as being at the beginning of a term.
Implied proximity is used in search fields indexed as single words,
for example, the Basic Index.

=> dup rem l4
DUPLICATE IS NOT AVAILABLE IN 'GENBANK'.
ANSWERS FROM THESE FILES WILL BE CONSIDERED UNIQUE
PROCESSING COMPLETED FOR L4
L5 47 DUP REM L4 (2 DUPLICATES REMOVED)

=> d ti l5 1-45

L5 ANSWER 1 OF 47 USPATFULL on STN DUPLICATE 1
TI Type II restriction endonuclease and application thereof

L5 ANSWER 2 OF 47 USPATFULL on STN
TI Genes of an otitis media isolate of haemophilus influenzae

L5 ANSWER 3 OF 47 USPATFULL on STN
TI H. pylori fucosyltransferases

L5 ANSWER 4 OF 47 USPATFULL on STN
TI Microorganisms and assays for the identification of antibiotics

L5 ANSWER 5 OF 47 USPATFULL on STN
TI Computer based versatile method for identifying protein coding DNA
sequences useful as drug targets

L5 ANSWER 6 OF 47 USPATFULL on STN
TI Methods for high throughput genome analysis using restriction site
tagged microarrays

L5 ANSWER 7 OF 47 USPATFULL on STN
TI Proteins, in particular membrane proteins, of Helicobacter pylori, their
preparation and use

L5 ANSWER 8 OF 47 USPATFULL on STN
TI Nucleic acid and amino acid sequences relating to Helicobacter pylori

for diagnostics and therapeutics

L5 ANSWER 9 OF 47 USPATFULL on STN
TI Plasmid DNA from *Yersinia pestis*

L5 ANSWER 10 OF 47 CAPLUS COPYRIGHT 2007 ACS on STN DUPLICATE 2
TI Isolation and Characterization of a HpyC1I Restriction-Modification System in *Helicobacter pylori*

L5 ANSWER 11 OF 47 USPATFULL on STN
TI dapE gene of *Helicobacter pylori* and dapE- mutant strains of *Helicobacter pylori*

L5 ANSWER 12 OF 47 USPATFULL on STN
TI *Helicobacter pylori* antigen

L5 ANSWER 13 OF 47 USPATFULL on STN
TI dapE gene on *Helicobacter pylori* and dapE- mutant strains of *Helicobacter pylori*

L5 ANSWER 14 OF 47 USPATFULL on STN
TI Nucleotide sequence of the *Mycoplasma genitalium* genome, fragments thereof, and uses thereof

L5 ANSWER 15 OF 47 USPATFULL on STN
TI Bacterial antigens and vaccine compositions

L5 ANSWER 16 OF 47 USPATFULL on STN
TI Microorganisms and assays for the identification of antibiotics

L5 ANSWER 17 OF 47 USPATFULL on STN
TI DNA adenine methyltransferases and uses thereof

L5 ANSWER 18 OF 47 USPATFULL on STN
TI RECOMBINANT MICROORGANISMS EXPRESSING ANTIGENIC PROTEINS OF *HELICOBACTER PYLORI*

L5 ANSWER 19 OF 47 USPATFULL on STN
TI Compositions and methods relating to drug discovery and detection and treatment of gastrointestinal diseases

L5 ANSWER 20 OF 47 USPATFULL on STN
TI Bacterial antigens and vaccine compositions

L5 ANSWER 21 OF 47 USPATFULL on STN
TI Compositions comprising isolated *Helicobacter pylori* CagI polynucleotides and method of preparation thereof

L5 ANSWER 22 OF 47 USPATFULL on STN
TI *Helicobacter* TagA gene fusion protein

L5 ANSWER 23 OF 47 USPATFULL on STN
TI Purified vacuolating toxin from *Helicobacter pylori* and methods to use same

L5 ANSWER 24 OF 47 USPATFULL on STN
TI Immunogenic compositions against *Helicobacter* infection, polypeptides for use in the compositions, and nucleic acid sequences encoding said polypeptides

L5 ANSWER 25 OF 47 USPATFULL on STN
TI Nucleotide sequences coding for a protein with urease activity

L5 ANSWER 26 OF 47 USPATFULL on STN
TI Vacuolating toxin-deficient *H. pylori*

L5 ANSWER 27 OF 47 USPATFULL on STN
 TI Taga gene and methods for detecting predisposition to peptic ulceration

L5 ANSWER 28 OF 47 GENBANK® COPYRIGHT 2007 on STN
 TITLE (TI): The complete genome sequence of the European
 Francisella tularensis subspecies tularensis isolate
 FSC 198 suggests that it is derived from the archetypal
 laboratory strain Schu S4, originally isolated in North
 America
 TITLE (TI): Direct Submission

L5 ANSWER 29 OF 47 GENBANK® COPYRIGHT 2007 on STN
 TITLE (TI): Who ate whom? Adaptive Helicobacter genomic changes
 that accompanied a host jump from early humans to large
 felines
 TITLE (TI): Direct Submission

L5 ANSWER 30 OF 47 GENBANK® COPYRIGHT 2007 on STN
 TITLE (TI): Extensive DNA inversions in the B. fragilis genome
 control variable gene expression
 TITLE (TI): Direct Submission

L5 ANSWER 31 OF 47 GENBANK® COPYRIGHT 2007 on STN
 TITLE (TI): The Complete Genome Sequence of Neisseria gonorrhoeae
 TITLE (TI): Direct Submission

L5 ANSWER 32 OF 47 GENBANK® COPYRIGHT 2007 on STN
 TITLE (TI): The complete genome sequence of Francisella tularensis,
 the causative agent of tularemia
 TITLE (TI): Direct Submission

L5 ANSWER 33 OF 47 GENBANK® COPYRIGHT 2007 on STN
 TITLE (TI): Genome sequence of Streptococcus mutans UA159, a
 cariogenic dental pathogen
 TITLE (TI): Direct Submission

L5 ANSWER 34 OF 47 GENBANK® COPYRIGHT 2007 on STN
 TITLE (TI): Genome Sequence of Yersinia pestis KIM
 TITLE (TI): Direct Submission

L5 ANSWER 35 OF 47 GENBANK® COPYRIGHT 2007 on STN
 TITLE (TI): The genome sequence of the food-borne pathogen
 Campylobacter jejuni reveals hypervariable sequences
 TITLE (TI): Re-annotation of Campylobacter jejuni NCTC11168
 TITLE (TI): Direct Submission
 TITLE (TI): Direct Submission

L5 ANSWER 36 OF 47 GENBANK® COPYRIGHT 2007 on STN
 TITLE (TI): Complete nucleotide sequence of the prophage VT2-Sakai
 carrying the verotoxin 2 genes of the enterohemorrhagic
 Escherichia coli O157:H7 derived from the Sakai
 outbreak
 TITLE (TI): Comparative analysis of the whole set of rRNA operons
 between an enterohemorrhagic Escherichia coli O157:H7
 Sakai strain and an Escherichia coli K-12 strain MG1655

TITLE (TI): Complete nucleotide sequence of the prophage VT1-Sakai carrying the Shiga toxin 1 genes of the enterohemorrhagic Escherichia coli O157:H7 strain derived from the Sakai outbreak

TITLE (TI): Complete genome sequence of enterohemorrhagic Escherichia coli O157:H7 and genomic comparison with a laboratory strain K-12

TITLE (TI): Direct Submission

L5 ANSWER 37 OF 47 GENBANK® COPYRIGHT 2007 on STN

TITLE (TI): Genomic plasticity of the causative agent of melioidosis, Burkholderia pseudomallei

TITLE (TI): Direct Submission

L5 ANSWER 38 OF 47 GENBANK® COPYRIGHT 2007 on STN

TITLE (TI): Insights into the evolution of Yersinia pestis through whole-genome comparison with Yersinia pseudotuberculosis

TITLE (TI): Direct Submission

L5 ANSWER 39 OF 47 GENBANK® COPYRIGHT 2007 on STN

TITLE (TI): The genome sequence of the enterobacterial phytopathogen Erwinia carotovora subsp. atroseptica SCRI1043 and functional genomic identification of novel virulence factors

TITLE (TI): Direct Submission

L5 ANSWER 40 OF 47 GENBANK® COPYRIGHT 2007 on STN

TITLE (TI): Complete genomes of two clinical Staphylococcus aureus strains: evidence for the rapid evolution of virulence and drug resistance

TITLE (TI): Direct Submission

L5 ANSWER 41 OF 47 GENBANK® COPYRIGHT 2007 on STN

TITLE (TI): Complete genomes of two clinical Staphylococcus aureus strains: evidence for the rapid evolution of virulence and drug resistance

TITLE (TI): Direct Submission

L5 ANSWER 42 OF 47 GENBANK® COPYRIGHT 2007 on STN

TITLE (TI): Complete genome sequence of an M1 strain of Streptococcus pyogenes

TITLE (TI): Direct Submission

L5 ANSWER 43 OF 47 GENBANK® COPYRIGHT 2007 on STN

TITLE (TI): Genome sequence of enterohaemorrhagic Escherichia coli O157:H7

TITLE (TI): Direct Submission

L5 ANSWER 44 OF 47 GENBANK® COPYRIGHT 2007 on STN

TITLE (TI): Complete DNA sequence of a serogroup A strain of Neisseria meningitidis Z2491

TITLE (TI): Direct Submission

L5 ANSWER 45 OF 47 GENBANK® COPYRIGHT 2007 on STN

TITLE (TI): Complete DNA sequence of a serogroup A strain of

TITLE (TI): Neisseria meningitidis Z2491
Direct Submission

=> d ti 15 46-47

L5 ANSWER 46 OF 47 GENBANK® COPYRIGHT 2007 on STN

TITLE (TI): Complete DNA sequence of a serogroup A strain of
Neisseria meningitidis Z2491
TITLE (TI): Direct Submission

L5 ANSWER 47 OF 47 GENBANK® COPYRIGHT 2007 on STN

TITLE (TI): The genome sequence of the food-borne pathogen
Campylobacter jejuni reveals hypervariable sequences
TITLE (TI): Direct Submission

=> s 13 and (bcc? or ccattc?)

L6 31 L3 AND (BCC? OR CCATC?)

=> dup rem 16

DUPLICATE IS NOT AVAILABLE IN 'GENBANK'.
ANSWERS FROM THESE FILES WILL BE CONSIDERED UNIQUE
PROCESSING COMPLETED FOR L6

L7 29 DUP REM L6 (2 DUPLICATES REMOVED)

=> d 17 1-29

L7 ANSWER 1 OF 29 USPATFULL on STN DUPLICATE 1

AN 2005:233506 USPATFULL

TI Type II restriction endonuclease and application thereof

IN Wang, Jin-Town, Taipei, TAIWAN, PROVINCE OF CHINA

Lin, Tzu-Lung, Taipei, TAIWAN, PROVINCE OF CHINA

PI US 2005202443 A1 20050915

AI US 2004-796669 A1 20040309 (10)

DT Utility

FS APPLICATION

LN.CNT 612

INCL INCLM: 435/006.000

INCLS: 435/199.000; 435/252.300; 435/471.000; 536/023.200

NCL NCLM: 435/006.000

NCLS: 435/199.000; 435/252.300; 435/471.000; 536/023.200

IC [7]

ICM C12Q001-68

ICS C07H021-04; C12N009-10; C12N015-74

IPCI C12Q0001-68 [ICM,7]; C07H0021-04 [ICS,7]; C07H0021-00 [ICS,7,C*];

C12N0009-10 [ICS,7]; C12N0015-74 [ICS,7]

IPCR C07H0021-00 [I,C*]; C07H0021-04 [I,A]; C12N0009-10 [I,C*];

C12N0009-10 [I,A]; C12N0015-74 [I,C*]; C12N0015-74 [I,A];

C12Q0001-68 [I,C*]; C12Q0001-68 [I,A]

CAS INDEXING IS AVAILABLE FOR THIS PATENT.

L7 ANSWER 2 OF 29 USPATFULL on STN

AN 2005:189426 USPATFULL

TI H. pylori fucosyltransferases

IN Simala-Grant, Joanne, Edmonton, CANADA

Taylor, Diane, Edmonton, CANADA

Johnson, Karl F., Hatboro, PA, UNITED STATES

Bezila, Daniel James, Philadelphia, PA, UNITED STATES

PA Neose Technologies, Inc., Horsham, PA, UNITED STATES (non-U.S.
corporation)

Governors of the University of Alberta, Edmonton, CANADA (non-U.S.
corporation)

PI US 2005164338 A1 20050728
 AI US 2004-764212 A1 20040122 (10)
 DT Utility
 FS APPLICATION
 LN.CNT 4386
 INCL INCLM: 435/068.100
 INCLS: 530/395.000; 435/193.000; 435/320.100; 435/325.000
 NCL NCLM: 435/068.100
 NCLS: 435/193.000; 435/320.100; 435/325.000; 530/395.000
 IC [7]
 ICM C12P021-06
 ICS C12N009-10
 IPCI C12P0021-06 [ICM,7]; C12N0009-10 [ICS,7]
 IPCR C12N0009-10 [I,C*]; C12N0009-10 [I,A]; C12P0021-06 [I,C*];
 C12P0021-06 [I,A]

CAS INDEXING IS AVAILABLE FOR THIS PATENT.

L7 ANSWER 3 OF 29 USPATFULL on STN
 AN 2005:183455 USPATFULL
 TI Microorganisms and assays for the identification of antibiotics
 IN Yocum, R. Rogers, Lexington, MA, UNITED STATES
 Patterson, Thomas A., North Attleboro, MA, UNITED STATES
 PA OmniGene Bioproducts, Inc., Cambridge, MA, UNITED STATES, 02138 (U.S. corporation)
 PI US 2005158842 A1 20050721
 AI US 2004-11979 A1 20041213 (11)
 RLI Division of Ser. No. US 2001-813453, filed on 20 Mar 2001, GRANTED, Pat. No. US 6830898
 PRAI US 2000-227860P 20000824 (60)
 DT Utility
 FS APPLICATION
 LN.CNT 4666
 INCL INCLM: 435/252.300
 INCLS: 435/471.000; 536/023.200
 NCL NCLM: 435/252.300
 NCLS: 435/471.000; 536/023.200
 IC [7]
 ICM C12N001-21
 ICS C07H021-04; C12N015-74
 IPCI C12N0001-21 [ICM,7]; C07H0021-04 [ICS,7]; C07H0021-00 [ICS,7,C*];
 C12N0015-74 [ICS,7]
 IPCR C12N0009-12 [I,C*]; C12N0009-12 [I,A]; C12N0015-52 [I,C*];
 C12N0015-52 [I,A]; C12N0015-54 [I,C*]; C12N0015-54 [I,A];
 C12P0013-00 [I,C*]; C12P0013-02 [I,A]; C12P0017-02 [I,C*];
 C12P0017-04 [I,A]

CAS INDEXING IS AVAILABLE FOR THIS PATENT.

L7 ANSWER 4 OF 29 USPATFULL on STN
 AN 2005:158272 USPATFULL
 TI Computer based versatile method for identifying protein coding DNA sequences useful as drug targets
 IN Brahmachari, Samir Kumar, Delhi, INDIA
 Dash, Debasis, Delhi, INDIA
 Sharma, Ramakant, Delhi, INDIA
 Maheshwari, Jitendra Kumar, Delhi, INDIA
 PI US 2005136480 A1 20050623
 AI US 2004-755415 A1 20040113 (10)
 RLI Continuation-in-part of Ser. No. US 2003-727989, filed on 5 Dec 2003, PENDING
 DT Utility
 FS APPLICATION
 LN.CNT 9116
 INCL INCLM: 435/007.100
 INCLS: 702/019.000
 NCL NCLM: 435/007.100

NCLS: 702/019.000
IC [7]
ICM G01N033-53
ICS G06F019-00; G01N033-48; G01N033-50
IPCI G01N0033-53 [ICM,7]; G06F0019-00 [ICS,7]; G01N0033-48 [ICS,7];
G01N0033-50 [ICS,7]
IPCR G01N0033-48 [I,C*]; G01N0033-48 [I,A]; G01N0033-50 [I,C*];
G01N0033-50 [I,A]; G01N0033-53 [I,C*]; G01N0033-53 [I,A];
G06F0019-00 [I,C*]; G06F0019-00 [I,A]

CAS INDEXING IS AVAILABLE FOR THIS PATENT.

L7 ANSWER 5 OF 29 USPATFULL on STN
AN 2004:65910 USPATFULL
TI Plasmid DNA from Yersinia pestis
IN Blattner, Frederick R., Madison, WI, United States
Burland, Valerie, Cross Plains, WI, United States
Rose, Debra J., Fond du Lac, WI, United States
Mayhew, George F., Madison, WI, United States
Perna, Nicole, Madison, WI, United States
Perry, Robert D, Lexington, KY, United States
Straley, Susan C, Lexington, KY, United States
Fetherston, Jacqueline D., Lexington, KY, United States
Lindler, Luther E., Wheaton, MD, United States
Plano, Gregory V., Miami, FL, United States
PA Wisconsin Alumni Research Foundation, Madison, WI, United States (U.S.
corporation)
PI US 6706522 B1 20040316
AI US 1999-409800 19990930 (9)
DT Utility
FS GRANTED
LN.CNT 4492
INCL INCLM: 435/320.100
INCLS: 435/252.300; 536/023.100
NCL NCLM: 435/320.100
NCLS: 435/252.300; 536/023.100
IC [7]
ICM C12N015-63
IPCI C12N0015-63 [ICM,7]
IPCR C07K0014-195 [I,C*]; C07K0014-24 [I,A]
EXF 536/23.1; 435/320.1; 435/252.3
CAS INDEXING IS AVAILABLE FOR THIS PATENT.

L7 ANSWER 6 OF 29 CAPLUS COPYRIGHT 2007 ACS on STN DUPLICATE 2
AN 2004:218217 CAPLUS
DN 140:333344
TI Isolation and Characterization of a HpyC1I Restriction-Modification System
in Helicobacter pylori
AU Lin, Tzu-Lung; Shun, Chia-Tun; Chang, Kai-Chih; Wang, Jin-Town
CS College of Medicine, Graduate Institute of Microbiology, National Taiwan
University, Taipei, 10016, Taiwan
SO Journal of Biological Chemistry (2004), 279(12), 11156-11162
CODEN: JBCHA3; ISSN: 0021-9258
PB American Society for Biochemistry and Molecular Biology
DT Journal
LA English
RE.CNT 26 THERE ARE 26 CITED REFERENCES AVAILABLE FOR THIS RECORD
ALL CITATIONS AVAILABLE IN THE RE FORMAT

L7 ANSWER 7 OF 29 USPATFULL on STN
AN 2003:81597 USPATFULL
TI Nucleotide sequence of the mycoplasma genitalium genome, fragments
thereof, and uses thereof
IN Fraser, Claire M., Potomac, MD, United States
Adams, Mark D., N. Potomac, MD, United States
Gocayne, Jeannine D., Silver Spring, MD, United States

Hutchison, III, Clyde A., Chapel Hill, NC, United States
 Smith, Hamilton O., Towson, MD, United States
 Venter, J. Craig, Potomac, MD, United States
 White, Owen, Gaithersburg, MD, United States
 PA The Institute for Genomic Research, Rockville, MD, United States (U.S. corporation)
 Johns Hopkins University, Baltimore, MD, United States (U.S. corporation)
 The University of North Carolina at Chapel Hill, Chapel Hill, NC, United States (U.S. corporation)
 PI US 6537773 B1 20030325
 AI US 1995-545528 19951019 (8)
 RLI Continuation-in-part of Ser. No. US 1995-488018, filed on 7 Jun 1995, now abandoned Continuation-in-part of Ser. No. US 1995-473545, filed on 7 Jun 1995, now abandoned
 DT Utility
 FS GRANTED
 LN.CNT 15190
 INCL INCLM: 435/069.100
 INCLS: 536/023.700; 536/024.320; 435/252.300; 435/320.100
 NCL NCLM: 435/069.100
 NCLS: 435/252.300; 435/320.100; 536/023.700; 536/024.320
 IC [7]
 ICM C12Q001-68
 IPCI C12Q0001-68 [ICM,7]
 IPCR A61K0038-00 [N,C*]; A61K0038-00 [N,A]; C07K0014-195 [I,C*]; C07K0014-30 [I,A]
 EXP 536/23.7; 536/23.1; 536/24.3; 536/24; 536/52; 435/69.1; 435/320.1
 CAS INDEXING IS AVAILABLE FOR THIS PATENT.

L7 ANSWER 8 OF 29 USPATFULL on STN
 AN 2002:301138 USPATFULL
 TI Microorganisms and assays for the identification of antibiotics
 IN Yocum, R. Rogers, Lexington, MA, UNITED STATES
 Patterson, Thomas A., North Attleboro, MA, UNITED STATES
 PI US 2002168681 A1 20021114
 US 6830898 B2 20041214
 AI US 2001-813453 A1 20010320 (9)
 PRAI US 2000-227860P 20000824 (60)
 DT Utility
 FS APPLICATION
 LN.CNT 4858
 INCL INCLM: 435/007.100
 NCL NCLM: 435/032.000; 435/007.100
 NCLS: 424/009.200; 435/007.100; 514/001.000; 530/300.000; 530/350.000
 IC [7]
 ICM G01N033-53
 IPCI G01N0033-53 [ICM,7]
 IPCI-2 C12Q0001-18 [ICM,7]; A01N0061-00 [ICS,7]; C07K0002-00 [ICS,7]; C07K0014-195 [ICS,7]; A61K0049-00 [ICS,7]
 IPCR C12N0009-12 [I,C*]; C12N0009-12 [I,A]; C12N0015-52 [I,C*]; C12N0015-52 [I,A]; C12N0015-54 [I,C*]; C12N0015-54 [I,A]; C12P0013-00 [I,C*]; C12P0013-02 [I,A]; C12P0017-02 [I,C*]; C12P0017-04 [I,A]
 CAS INDEXING IS AVAILABLE FOR THIS PATENT.

L7 ANSWER 9 OF 29 USPATFULL on STN
 AN 2000:57536 USPATFULL
 TI Compositions and methods relating to drug discovery and detection and treatment of gastrointestinal diseases
 IN Corthesy-Theulaz, Irene, Epalinges, Switzerland
 PA Kieta Holding SA, St-Prex, Switzerland (non-U.S. corporation)
 PI US 6060241 20000509
 AI US 1997-834776 19970403 (8)
 PRAI US 1996-14906P 19960405 (60)

DT Utility
FS Granted
LN.CNT 2585
INCL INCLM: 435/006.000
INCLS: 536/023.200
NCL NCLM: 435/006.000
NCLS: 536/023.200
IC [7]
ICM C12Q001-70
IPCI C12Q0001-70 [ICM,7]
IPCR A61K0038-00 [N,A]; A61K0038-00 [N,C*]; C12N0009-00 [I,A];
C12N0009-00 [I,C*]; C12N0009-10 [I,A]; C12N0009-10 [I,C*];
C12Q0001-68 [I,A]; C12Q0001-68 [I,C*]
EXF 536/23.2; 435/6
CAS INDEXING IS AVAILABLE FOR THIS PATENT.

L7 ANSWER 10 OF 29 USPATFULL on STN
AN 1999:85216 USPATFULL
TI Compositions comprising isolated Helicobacter pylori CagI
polynucleotides and method of preparation thereof
IN Covacci, Antonello, Siena, Italy
PA Chiron S.p.A., Italy (non-U.S. corporation)
PI US 5928865 19990727
AI US 1995-477451 19950607 (8)
RLI Continuation-in-part of Ser. No. US 1995-425194, filed on 20 Apr 1995,
now abandoned And Ser. No. US 1995-471491, filed on 6 Jun 1995 which is
a division of Ser. No. US 256848
PRAI IT 1992-FI52 19920302
DT Utility
FS Granted
LN.CNT 6155
INCL INCLM: 435/006.000
INCLS: 435/007.320; 536/023.100
NCL NCLM: 435/006.000
NCLS: 435/007.320; 536/023.100
IC [6]
ICM C12Q001-68
IPCI C12Q0001-68 [ICM,6]
IPCR A61K0038-00 [N,C*]; A61K0038-00 [N,A]; A61K0039-00 [N,C*];
A61K0039-00 [N,A]; C07K0014-195 [I,C*]; C07K0014-205 [I,A];
C12Q0001-68 [I,C*]; C12Q0001-68 [I,A]
EXF 435/7.32; 435/6; 536/23.1
CAS INDEXING IS AVAILABLE FOR THIS PATENT.

L7 ANSWER 11 OF 29 USPATFULL on STN
AN 1998:150478 USPATFULL
TI Immunogenic compositions against helicobacter infection, polypeptides
for use in the compositions, and nucleic acid sequences encoding said
polypeptides
IN Labigne, Agnes, Bures S/Yvette, France
Suerbaum, Sebastin, Bochum, Germany, Federal Republic of
Ferrero, Richard L., Paris, France
Thiberge, Jean-Michel, Plaisir, France
PA Institut Pasteur, Paris, France (non-U.S. corporation)
Institut National de la Sante et de la Recherche Medicale, Paris, France
(non-U.S. corporation)
PI US 5843460 19981201
AI US 1995-467822 19950606 (8)
RLI Continuation of Ser. No. US 1995-447177, filed on 19 May 1995 which is a
continuation-in-part of Ser. No. US 1995-432697, filed on 2 May 1995
PRAI EP 1993-401309 19930519
WO 1993-EP3259 19931119
DT Utility
FS Granted
LN.CNT 3594

INCL INCLM: 424/234.100
 INCLS: 435/007.320; 435/006.000; 435/007.900; 514/234.500; 514/041.000
 NCL NCLM: 424/234.100
 NCLS: 435/006.000; 435/007.320; 435/007.900; 514/041.000; 514/234.500
 IC [6]
 ICM A61K039-02
 IPCI A61K0039-02 [ICM,6]
 IPCR A61K0039-00 [N,C*]; A61K0039-00 [N,A]; C07K0014-195 [I,C*];
 C07K0014-205 [I,A]; C07K0016-12 [I,C*]; C07K0016-12 [I,A];
 C12N0009-78 [I,C*]; C12N0009-80 [I,A]; C12Q0001-68 [I,C*];
 C12Q0001-68 [I,A]
 EXF 435/7.32; 435/4; 435/6; 435/7.9; 514/234.5; 514/41; 424/234.1
 CAS INDEXING IS AVAILABLE FOR THIS PATENT.

L7 ANSWER 12 OF 29 GENBANK® COPYRIGHT 2007 on STN

LOCUS (LOC): AM286280 GenBank (R)
 GenBank ACC. NO. (GBN): AM286280
 GenBank VERSION (VER): AM286280.1 GI:110319990
 SEQUENCE LENGTH (SQL): 1892616
 MOLECULE TYPE (CI): DNA; circular
 DIVISION CODE (CI): Bacteria
 DATE (DATE): 12 Jul 2006
 DEFINITION (DEF): Francisella tularensis subsp. tularensis strain FSC 198
 complete genome.
 KEYWORDS (ST): complete genome
 SOURCE: Francisella tularensis subsp. tularensis FSC 198
 ORGANISM (ORGN): Francisella tularensis subsp. tularensis FSC 198
 Bacteria; Proteobacteria; Gammaproteobacteria;
 Thiotrichales; Francisellaceae; Francisella
 REFERENCE: 1
 AUTHOR (AU): Chaudhuri, R.R.; Ren, C.P.; Desmond, L.; Vincent, G.A.;
 Silman, N.J.; Brehm, J.; Elmore, M.J.; Hudson, M.J.;
 Forsman, M.; Isherwood, K.E.; Gurycova, D.; Minton, N.P.;
 Titball, R.W.; Pallen, M.J.; Vipond, R.
 TITLE (TI): The complete genome sequence of the European
 Francisella tularensis subspecies tularensis isolate
 FSC 198 suggests that it is derived from the archetypal
 laboratory strain Schu S4, originally isolated in North
 America
 JOURNAL (SO): Unpublished
 REFERENCE: 2 (bases 1 to 1892616)
 AUTHOR (AU): Chaudhuri, R.R.
 TITLE (TI): Direct Submission
 JOURNAL (SO): Submitted (04-JUL-2006) Chaudhuri R.R., Division of
 Immunity and Infection, University of Birmingham,
 Vincent Drive, Edgbaston, Birmingham, B15 2TT, UNITED
 KINGDOM

FEATURES (FEAT):

| Feature Key | Location | Qualifier |
|-------------|------------|--|
| source | 1..1892616 | /organism="Francisella tularensis subsp. tularensis FSC 198" /mol-type="genomic DNA" /strain="FSC 198" /sub-species="tularensis" /db-xref="taxon:393115" /country="Slovakia" |

L7 ANSWER 13 OF 29 GENBANK® COPYRIGHT 2007 on STN

LOCUS (LOC): AM260522 GenBank (R)
 GenBank ACC. NO. (GBN): AM260522

GenBank VERSION (VER): AM260522.1 GI:109713861
 CAS REGISTRY NO. (RN): 899490-11-0
 SEQUENCE LENGTH (SQL): 1553927
 MOLECULE TYPE (CI): DNA; circular
 DIVISION CODE (CI): Bacteria
 DATE (DATE): 14 Nov 2006
 DEFINITION (DEF): *Helicobacter acinonychis* str. Sheeba complete genome,
 strain Sheeba.
 KEYWORDS (ST): complete genome
 SOURCE: *Helicobacter acinonychis* str. Sheeba
 ORGANISM (ORGN): *Helicobacter acinonychis* str. Sheeba
 Bacteria; Proteobacteria; Epsilonproteobacteria;
 Campylobacteriales; Helicobacteraceae; Helicobacter
 COMMENT:
 Clone requests: scs@bx.psu.edu.
 REFERENCE: 1
 AUTHOR (AU): Eppinger, M.; Baar, C.; Linz, B.; Raddatz, G.; Lanz, C.;
 Keller, H.; Morelli, G.; Gressmann, H.; Achtman, M.;
 Schuster, S.C.
 TITLE (TI): Who ate whom? Adaptive *Helicobacter* genomic changes
 that accompanied a host jump from early humans to large
 felines
 JOURNAL (SO): PLoS Genet., 2 (7), E120 (2006)
 REFERENCE: 2 (bases 1 to 1553927)
 AUTHOR (AU): Schuster, S.C.
 TITLE (TI): Direct Submission
 JOURNAL (SO): Submitted (27-MAR-2006) Schuster S.C., Department of
 Biochemistry and Molecular Biology, Center for
 Comparative Genomics and Bioinformatics Center for
 Infectious Disease Dynamics, 310 Wartik Building, Penn
 State University, University Park, PA 16802, USA Phone
 +1 814 863-9278, FAX +1 814 863-6699

| FEATURES (FEAT): | Feature Key | Location | Qualifier |
|-------------------|-------------|------------|---|
| =====+=====+===== | source | 1..1553927 | /organism="Helicobacter acinonychis str. Sheeba" /mol-type="genomic DNA" /strain="Sheeba" /db-xref="taxon:382638" |

L7 ANSWER 14 OF 29 GENBANK® COPYRIGHT 2007 on STN

LOCUS (LOC): CR626927 GenBank (R)
 GenBank ACC. NO. (GBN): CR626927
 GenBank VERSION (VER): CR626927.1 GI:60491031
 CAS REGISTRY NO. (RN): 843924-26-5
 SEQUENCE LENGTH (SQL): 5205140
 MOLECULE TYPE (CI): DNA; circular
 DIVISION CODE (CI): Bacteria
 DATE (DATE): 17 Apr 2005
 DEFINITION (DEF): *Bacteroides fragilis* NCTC 9343, complete genome.
 KEYWORDS (ST): complete genome
 SOURCE: *Bacteroides fragilis* NCTC 9343
 ORGANISM (ORGN): *Bacteroides fragilis* NCTC 9343
 Bacteria; Bacteroidetes; Bacteroides (class);
 Bacteroidales; Bacteroidaceae; Bacteroides
 REFERENCE: 1 (bases 1 to 5205140)
 AUTHOR (AU): Cerdeno-Tarraga, A.M.; Patrick, S.; Crossman, L.C.;
 Blakely, G.; Abratt, V.; Lennard, N.; Poxton, I.;
 Duerden, B.; Harris, B.; Quail, M.A.; Barron, A.; Clark, L.;
 Corton, C.; Doggett, J.; Holden, M.T.; Larke, N.; Line, A.;
 Lord, A.; Norbertczak, H.; Ormond, D.; Price, C.;

TITLE (TI): Rabbinowitsch,E.; Woodward,J.; Barrell,B.; Parkhill,J.
 Extensive DNA inversions in the B. fragilis genome
 control variable gene expression
 JOURNAL (SO): Science, 307 (5714), 1463-1465 (2005)
 OTHER SOURCE (OS): CA 142:234199
 REFERENCE: 2 (bases 1 to 5205140)
 AUTHOR (AU): Cerdeno-Tarraga,A.M.
 TITLE (TI): Direct Submission
 JOURNAL (SO): Submitted (29-JUL-2004) Cerdeno-Tarraga A.M., submitted
 on behalf of the Pathogen Sequencing Unit, Sanger
 Institute, Wellcome Trust Genome Campus, Hinxton,
 Cambridge CB10 1SA E-mail: amct@sanger.ac.uk

FEATURES (FEAT):

| Feature Key | Location | Qualifier |
|-------------|------------|---|
| source | 1..5205140 | /organism="Bacteroides fragilis NCTC 9343" /mol-type="genomic DNA" /strain="ATCC 25285 = NCTC 9343" /db-xref="taxon:272559" |

L7 ANSWER 15 OF 29 GENBANK® COPYRIGHT 2007 on STN

LOCUS (LOC): AE004969 GenBank (R)
 GenBank ACC. NO. (GBN): AE004969
 GenBank VERSION (VER): AE004969.1 GI:59717368
 CAS REGISTRY NO. (RN): 432023-66-0
 SEQUENCE LENGTH (SQL): 2153922
 MOLECULE TYPE (CI): DNA; circular
 DIVISION CODE (CI): Bacteria
 DATE (DATE): 14 Feb 2005
 DEFINITION (DEF): Neisseria gonorrhoeae FA 1090, complete genome.
 SOURCE: Neisseria gonorrhoeae FA 1090
 ORGANISM (ORGN): Neisseria gonorrhoeae FA 1090
 Bacteria; Proteobacteria; Betaproteobacteria;
 Neisseriales; Neisseriaceae; Neisseria
 REFERENCE: 1 (bases 1 to 2153922)
 AUTHOR (AU): Lewis,L.A.; Gillaspay,A.F.; McLaughlin,R.E.; Gipson,M.;
 Ducey,T.F.; Ownbey,T.; Hartman,K.; Nydick,C.;
 Carson,M.B.; Vaughn,J.; Thomson,C.; Song,L.; Lin,S.;
 Yuan,X.; Najjar,F.; Zhan,M.; Ren,Q.; Zhu,H.; Qi,S.;
 Kenton,S.M.; Lai,H.; White,J.D.; Clifton,S.; Roe,B.A.;
 Dyer,D.W.
 TITLE (TI): The Complete Genome Sequence of Neisseria gonorrhoeae
 JOURNAL (SO): Unpublished
 REFERENCE: 2 (bases 1 to 2153922)
 AUTHOR (AU): Lewis,L.A.; Gillaspay,A.F.; McLaughlin,R.E.; Gipson,M.;
 Ducey,T.F.; Ownbey,T.; Hartman,K.; Nydick,C.;
 Carson,M.B.; Vaughn,J.; Thomson,C.; Song,L.; Lin,S.;
 Yuan,X.; Najjar,F.; Zhan,M.; Ren,Q.; Zhu,H.; Qi,S.;
 Kenton,S.M.; Lai,H.; White,J.D.; Clifton,S.; Roe,B.A.;
 Dyer,D.W.
 TITLE (TI): Direct Submission
 JOURNAL (SO): Submitted (10-MAR-2003) Microbiology and Immunology,
 University of Oklahoma Health Sciences Center, 975 NE
 10th St., Oklahoma City, OK 73104, USA

FEATURES (FEAT):

| Feature Key | Location | Qualifier |
|-------------|------------|---|
| source | 1..2153922 | /organism="Neisseria gonorrhoeae FA 1090" /mol-type="genomic DNA" |

/strain="FA 1090"
/db-xref="taxon:242231"

L7 ANSWER 16 OF 29 GENBANK® COPYRIGHT 2007 on STN

LOCUS (LOC): AJ749949 GenBank (R)
GenBank ACC. NO. (GBN): AJ749949
GenBank VERSION (VER): AJ749949.1 GI:56603679
CAS REGISTRY NO. (RN): 799222-54-1
SEQUENCE LENGTH (SQL): 1892819
MOLECULE TYPE (CI): DNA; circular
DIVISION CODE (CI): Bacteria
DATE (DATE): 1 Mar 2006
DEFINITION (DEF): *Francisella tularensis* subsp. *tularensis* SCHU S4
complete genome.
KEYWORDS (ST): complete genome
SOURCE: *Francisella tularensis* subsp. *tularensis* SCHU S4
ORGANISM (ORGN): *Francisella tularensis* subsp. *tularensis* SCHU S4
Bacteria; Proteobacteria; Gammaproteobacteria;
Thiotrichales; Francisellaceae; *Francisella*
REFERENCE: 1
AUTHOR (AU): Larsson, P.; Oyston, P.C.; Chain, P.; Chu, M.C.;
Duffield, M.; Fuxelius, H.H.; Garcia, E.; Halltorp, G.;
Johansson, D.; Isherwood, K.E.; Karp, P.D.; Larsson, E.;
Liu, Y.; Michell, S.; Prior, J.; Prior, R.; Malfatti, S.;
Sjostedt, A.; Svensson, K.; Thompson, N.; Vergez, L.;
Wagg, J.K.; Wren, B.W.; Lindler, L.E.; Andersson, S.G.;
Forsman, M.; Titball, R.W.
TITLE (TI): The complete genome sequence of *Francisella tularensis*,
the causative agent of tularemia
JOURNAL (SO): Nat. Genet., 37 (2), 153-159 (2005)
REFERENCE: 2 (bases 1 to 1892819)
AUTHOR (AU): Duffield, M.L.
TITLE (TI): Direct Submission
JOURNAL (SO): Submitted (25-JUN-2004) Duffield M.L., Biomedical
Sciences, Defence Science and Technology Lab, Porton
Down, Wiltshire, SP4 0JQ, UNITED KINGDOM

FEATURES (FEAT):
Feature Key Location Qualifier
=====+=====+=====

| | | |
|--------|------------|---|
| source | 1..1892819 | /organism="Francisella tularensis subsp. tularensis SCHU S4" /mol-type="genomic DNA" /strain="SCHU S4" /sub-species="tularensis" /db-xref="taxon:177416" |
|--------|------------|---|

L7 ANSWER 17 OF 29 GENBANK® COPYRIGHT 2007 on STN

LOCUS (LOC): AE014133 GenBank (R)
GenBank ACC. NO. (GBN): AE014133 AE014853-AE015037
GenBank VERSION (VER): AE014133.1 GI:24378526
SEQUENCE LENGTH (SQL): 2030921
MOLECULE TYPE (CI): DNA; circular
DIVISION CODE (CI): Bacteria
DATE (DATE): 24 Jan 2006
DEFINITION (DEF): *Streptococcus mutans* UA159, complete genome.
SOURCE: *Streptococcus mutans* UA159
ORGANISM (ORGN): *Streptococcus mutans* UA159
Bacteria; Firmicutes; Lactobacillales;
Streptococcaceae; *Streptococcus*
COMMENT:

On or before Jan 18, 2006 this sequence version replaced

gi:24376380, gi:24376394, gi:24376399, gi:24376411, gi:24376427,
gi:24376440, gi:24376449, gi:24376457, gi:24376467, gi:24376477,
gi:24376489, gi:24376500, gi:24376508, gi:24376518, gi:24376529,
gi:24376540, gi:24376558, gi:24376568, gi:24376580, gi:24376598,
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gi:24377241, gi:24377253, gi:24377262, gi:24377272, gi:24377283,
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gi:24377479, gi:24377490, gi:24377501, gi:24377514, gi:24377528,
gi:24377540, gi:24377549, gi:24377559, gi:24377569, gi:24377578,
gi:24377588, gi:24377599, gi:24377613, gi:24377623, gi:24377640,
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gi:24377714, gi:24377718, gi:24377725, gi:24377743, gi:24377757,
gi:24377767, gi:24377778, gi:24377791, gi:24377802, gi:24377812,
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gi:24377876, gi:24377883, gi:24377895, gi:24377909, gi:24377922,
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gi:24377983, gi:24377998, gi:24378012, gi:24378027, gi:24378041,
gi:24378055, gi:24378065, gi:24378076, gi:24378090, gi:24378102,
gi:24378115, gi:24378119, gi:24378133, gi:24378147, gi:24378154,
gi:24378171, gi:24378183, gi:24378195, gi:24378206, gi:24378217,
gi:24378228, gi:24378240, gi:24378249, gi:24378266, gi:24378285,
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gi:24378472, gi:24378487, gi:24378500, gi:24378511, gi:24378520.

REFERENCE: 1 (bases 1 to 2030921)
AUTHOR (AU): Ajdic,D.; McShan,W.M.; McLaughlin,R.E.; Savic,G.;
Chang,J.; Carson,M.B.; Primeaux,C.; Tian,R.; Kenton,S.;
Jia,H.; Lin,S.; Qian,Y.; Li,S.; Zhu,H.; Najjar,F.;
Lai,H.; White,J.; Roe,B.A.; Ferretti,J.J.
TITLE (TI): Genome sequence of Streptococcus mutans UA159, a
cariogenic dental pathogen
JOURNAL (SO): Proc. Natl. Acad. Sci. U.S.A., 99 (22), 14434-14439
(2002)
OTHER SOURCE (OS): CA 137:364100
REFERENCE: 2 (bases 1 to 2030921)
AUTHOR (AU): Ajdic,D.; McShan,W.M.; McLaughlin,R.E.; Savic,G.;
Chang,J.; Carson,M.B.; Primeaux,C.; Tian,R.; Kenton,S.;
Jia,H.; Lin,S.; Qian,Y.; Li,S.; Zhu,H.; Najjar,F.;
Lai,H.; White,J.; Roe,B.A.; Ferretti,J.J.
TITLE (TI): Direct Submission
JOURNAL (SO): Submitted (09-JUL-2002) Department of Microbiology and
Immunology, University of Oklahoma Health Sciences
Center, 940 SL Young Blvd., Oklahoma City, OK 73104,
USA

FEATURES (FEAT):

| Feature Key | Location | Qualifier |
|-------------|------------|--|
| source | 1..2030921 | /organism="Streptococcus mutans UA159" /mol-type="genomic DNA" |

/strain="UA159"
/db-xref="taxon:210007"

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LOCUS (LOC): AE009952 GenBank (R)
GenBank ACC. NO. (GBN): AE009952 AE013601-AE014015
GenBank VERSION (VER): AE009952.1 GI:22002119
SEQUENCE LENGTH (SQL): 4600755
MOLECULE TYPE (CI): DNA; circular
DIVISION CODE (CI): Bacteria
DATE (DATE): 2 May 2006
DEFINITION (DEF): *Yersinia pestis* KIM, complete genome.
SOURCE: *Yersinia pestis* KIM
ORGANISM (ORGN): *Yersinia pestis* KIM
Bacteria; Proteobacteria; Gammaproteobacteria;
Enterobacteriales; Enterobacteriaceae; *Yersinia*

COMMENT:

On or before May 2, 2006 this sequence version replaced
gi:21956656, gi:21956667, gi:21956674, gi:21956680, gi:21956691,
gi:21956705, gi:21956717, gi:21956732, gi:21956743, gi:21956757,
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 gi:21961103, gi:21961114, gi:21961127, gi:21961139, gi:21961149.

REFERENCE: 1 (bases 1 to 4600755)
 AUTHOR (AU): Deng,W.; Burland,V.; Plunkett,G. III; Boutin,A.;
 Mayhew,G.F.; Liss,P.; Perna,N.T.; Rose,D.J.; Mau,B.;
 Zhou,S.; Schwartz,D.C.; Fetherston,J.D.; Lindler,L.E.;
 Brubaker,R.R.; Plana,G.V.; Straley,S.C.;
 McDonough,K.A.; Nilles,M.L.; Matson,J.S.;
 Blattner,F.R.; Perry,R.D.
 TITLE (TI): Genome Sequence of *Yersinia pestis* KIM
 JOURNAL (SO): J. Bacteriol., 184 (16), 4601-4611 (2002)
 OTHER SOURCE (OS): CA 137:120475
 REFERENCE: 2 (bases 1 to 4600755)
 AUTHOR (AU): Deng,W.; Burland,V.; Plunkett,G. III; Boutin,A.;
 Mayhew,G.F.; Liss,P.; Perna,N.T.; Rose,D.J.; Mau,B.;
 Zhou,S.; Schwartz,D.C.; Fetherston,J.D.; Lindler,L.E.;
 Brubaker,R.R.; Plana,G.V.; Straley,S.C.;
 McDonough,K.A.; Nilles,M.L.; Matson,J.S.;
 Blattner,F.R.; Perry,R.D.
 TITLE (TI): Direct Submission
 JOURNAL (SO): Submitted (21-FEB-2002) Genetics, University of
 Wisconsin, 445 Henry Mall, Madison, WI 53706, USA

FEATURES (FEAT):

| Feature Key | Location | Qualifier |
|-------------|------------|---|
| source | 1..4600755 | /organism="Yersinia pestis KIM" /mol-type="genomic DNA" /strain="KIM" |

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LOCUS (LOC): AL111168 GenBank (R)
 GenBank ACC. NO. (GBN): AL111168 AL139074 AL139075 AL139076 AL139077 AL139078
 AL139079
 GenBank VERSION (VER): AL111168.1 GI:30407139
 SEQUENCE LENGTH (SQL): 1641481
 MOLECULE TYPE (CI): DNA; circular
 DIVISION CODE (CI): Bacteria
 DATE (DATE): 14 Aug 2006
 DEFINITION (DEF): Campylobacter jejuni subsp. jejuni NCTC 11168 complete
 genome.
 KEYWORDS (ST): complete genome
 SOURCE: Campylobacter jejuni subsp. jejuni NCTC 11168
 ORGANISM (ORGN): Campylobacter jejuni subsp. jejuni NCTC 11168
 Bacteria; Proteobacteria; Epsilonproteobacteria;
 Campylobacteriales; Campylobacteraceae; Campylobacter

COMMENT:

On or before Aug 15, 2006 this sequence version replaced
 gi:6967505, gi:6967817, gi:6968128, gi:6968444, gi:6968723,
 gi:6968971.

Notes:

Details of C. jejuni sequencing at the Sanger Centre are available
 on the World Wide Web.

(URL, http://www.sanger.ac.uk/Projects/C_jejuni/).

REFERENCE:

1

AUTHOR (AU): Parkhill, J.; Wren, B.W.; Mungall, K.; Ketley, J.M.;
 Churcher, C.; Basham, D.; Chillingworth, T.; Davies, R.M.;
 Feltwell, T.; Holroyd, S.; Jagels, K.; Karlyshev, A.V.;
 Moule, S.; Pallen, M.J.; Penn, C.W.; Quail, M.A.;
 Rajandream, M.A.; Rutherford, K.M.; van Vliet, A.H.;
 Whitehead, S.; Barrell, B.G.

TITLE (TI): The genome sequence of the food-borne pathogen
 Campylobacter jejuni reveals hypervariable sequences

JOURNAL (SO): Nature, 403 (6770), 665-668 (2000)

OTHER SOURCE (OS): CA 132:147491

REFERENCE:

2

AUTHOR (AU): Gundogdu, O.; Bentley, S.D.; Dorrell, N.; Wren, B.W.;
 Parkhill, J.

TITLE (TI): Re-annotation of Campylobacter jejuni NCTC11168

JOURNAL (SO): Unpublished

REFERENCE:

3 (bases 1 to 1641481)

AUTHOR (AU): Parkhill, J.

TITLE (TI): Direct Submission

JOURNAL (SO): Submitted (09-FEB-2000) Submitted on behalf of the
 Campylobacter sequencing team, Sanger Centre, Wellcome
 Trust Genome Campus, Hinxton, Cambridge CB10 1SA
 E-mail: parkhill@sanger.ac.uk

REFERENCE:

4 (bases 1 to 1641481)

AUTHOR (AU): Gundogdu, O.

TITLE (TI): Direct Submission

JOURNAL (SO): Submitted (07-AUG-2006) Submitted on behalf of the
 Campylobacter sequencing team, Sanger Centre, Wellcome
 Trust Genome Campus, Hinxton, Cambridge CB10 1SA. In
 Collaboration with the Pathogen Molecular Biology
 Department at The London School of Hygiene & Tropical
 Medicine, London, Keppel Street, WC1E 7HT.
 E-mail: ozan.gundogdu@lshtm.ac.uk

FEATURES (FEAT):

| Feature Key | Location | Qualifier |
|-------------|----------|-----------|
|-------------|----------|-----------|

=====+=====+=====

source 1..1641481 /organism="Campylobacter jejuni
subsp. jejuni NCTC 11168"
/mol-type="genomic DNA"
/strain="NCTC 11168"
/sub-species="jejuni"
/db-xref="taxon:192222"

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LOCUS (LOC): BA000007 GenBank (R)
GenBank ACC. NO. (GBN): BA000007 AP002550-AP002569
GenBank VERSION (VER): BA000007.2 GI:47118301
CAS REGISTRY NO. (RN): 776960-28-2
SEQUENCE LENGTH (SQL): 5498450
MOLECULE TYPE (CI): DNA; circular
DIVISION CODE (CI): Bacteria
DATE (DATE): 10 Apr 2007
DEFINITION (DEF): Escherichia coli O157:H7 str. Sakai DNA, complete
genome.
SOURCE: Escherichia coli O157:H7 str. Sakai
ORGANISM (ORGN): Escherichia coli O157:H7 str. Sakai
Bacteria; Proteobacteria; Gammaproteobacteria;
Enterobacteriales; Enterobacteriaceae; Escherichia

COMMENT:

On or before Nov 5, 2004 this sequence version replaced
gi:13359456, gi:13359705, gi:13359995, gi:13360211, gi:13360491,
gi:13360886, gi:13361156, gi:13361466, gi:13361764, gi:13362012,
gi:13362333, gi:13362592, gi:13362858, gi:13363121, gi:13363382,
gi:13363693, gi:13363930, gi:13364198, gi:13364484, gi:13364704.
genome project

This work was done in collaboration with Tetsuya Hayashi, Makoto
Ohnishi, Keisuke Nakayama (Miyazaki Medical College), Kozo Makino,
Ken Kurokawa, Katsushi Yokoyama, Masashi Tanaka, Takeshi Honda,
Teruo Yasunaga, Hideo Shinagawa (Osaka University), Takahiro Murata
(Shinshu University), Chang-Gyun Han, Eiichi Ohtsubo, Toru Tobe,
Chihiro Sasakawa (University of Tokyo), Hideto Takami (Japan Marine
Science and Technology Center), Naotake Ogasawara (Nara Institute
of Science and Technology), Satoru Kuhara (Kyuushu University), and
supported by the Research for the Future Program of the Japan
Society for the Promotion of Science.

REFERENCE: 1
AUTHOR (AU): Makino, K.; Yokoyama, K.; Kubota, Y.; Yutsudo, C.H.;
Kimura, S.; Kurokawa, K.; Ishii, K.; Hattori, M.;
Tatsuno, I.; Abe, H.; Iida, T.; Yamamoto, K.; Onishi, M.;
Hayashi, T.; Yasunaga, T.; Honda, T.; Sasakawa, C.;
Shinagawa, H.
TITLE (TI): Complete nucleotide sequence of the prophage VT2-Sakai
carrying the verotoxin 2 genes of the enterohemorrhagic
Escherichia coli O157:H7 derived from the Sakai
outbreak
JOURNAL (SO): Genes Genet. Syst., 74 (5), 227-239 (1999)
OTHER SOURCE (OS): CA 134:37762
REFERENCE: 2
AUTHOR (AU): Ohnishi, M.; Murata, T.; Nakayama, K.; Kuhara, S.;
Hattori, M.; Kurokawa, K.; Yasunaga, T.; Yokoyama, K.;
Makino, K.; Shinagawa, H.; Hayashi, T.
TITLE (TI): Comparative analysis of the whole set of rRNA operons
between an enterohemorrhagic Escherichia coli O157:H7
Sakai strain and an Escherichia coli K-12 strain MG1655
JOURNAL (SO): Syst. Appl. Microbiol., 23 (3), 315-324 (2000)
OTHER SOURCE (OS): CA 134:263368
REFERENCE: 3
AUTHOR (AU): Yokoyama, K.; Makino, K.; Kubota, Y.; Watanabe, M.;
Kimura, S.; Yutsudo, C.H.; Kurokawa, K.; Ishii, K.;

Hattori,M.; Tatsuno,I.; Abe,H.; Yoh,M.; Iida,T.;
Ohnishi,M.; Hayashi,T.; Yasunaga,T.; Honda,T.;
Sasakawa,C.; Shinagawa,H.

TITLE (TI): Complete nucleotide sequence of the prophage VT1-Sakai
carrying the Shiga toxin 1 genes of the
enterohemorrhagic Escherichia coli O157:H7 strain
derived from the Sakai outbreak

JOURNAL (SO): Gene, 258 (1-2), 127-139 (2000)

OTHER SOURCE (OS): CA 135:71886

REFERENCE: 4

AUTHOR (AU): Hayashi,T.; Makino,K.; Ohnishi,M.; Kurokawa,K.;
Ishii,K.; Yokoyama,K.; Han,C.G.; Ohtsubo,E.;
Nakayama,K.; Murata,T.; Tanaka,M.; Tobe,T.; Iida,T.;
Takami,H.; Honda,T.; Sasakawa,C.; Ogasawara,N.;
Yasunaga,T.; Kuhara,S.; Shiba,T.; Hattori,M.;
Shinagawa,H.

TITLE (TI): Complete genome sequence of enterohemorrhagic
Escherichia coli O157:H7 and genomic comparison with a
laboratory strain K-12

JOURNAL (SO): DNA Res., 8 (1), 11-22 (2001)

OTHER SOURCE (OS): CA 134:217892

REFERENCE: 5 (bases 1 to 5498450)

AUTHOR (AU): Hattori,M.; Ishii,K.; Shiba,T.

TITLE (TI): Direct Submission

JOURNAL (SO): Submitted (26-JUN-2000) Masahira Hattori, Graduate
School of Frontier Sciences, University of Tokyo; 5-1-5
Kashiwanoha, Kashiwa, Chiba 277-8561, Japan
(E-mail:hattori@k.u-tokyo.ac.jp, Tel:81-4-7136-4070,
Fax:81-4-7136-4084)

FEATURES (FEAT):

| Feature Key | Location | Qualifier |
|-------------|------------|---|
| source | 1..5498450 | /organism="Escherichia coli O157:H7 str. Sakai" /mol-type="genomic DNA" /strain="Sakai" /sub-strain="RIMD 0509952" /serovar="O157:H7" /db-xref="taxon:386585" |

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LOCUS (LOC): BX571965 GenBank (R)

GenBank ACC. NO. (GBN): BX571965

GenBank VERSION (VER): BX571965.1 GI:52208053

CAS REGISTRY NO. (RN): 755924-52-8

SEQUENCE LENGTH (SQL): 4074542

MOLECULE TYPE (CI): DNA; circular

DIVISION CODE (CI): Bacteria

DATE (DATE): 17 Apr 2005

DEFINITION (DEF): Burkholderia pseudomallei strain K96243, chromosome 1,
complete sequence.

SOURCE: Burkholderia pseudomallei K96243

ORGANISM (ORGN): Burkholderia pseudomallei K96243
Bacteria; Proteobacteria; Betaproteobacteria;
Burkholderiales; Burkholderiaceae; Burkholderia;
pseudomallei group

REFERENCE: 1 (bases 1 to 4074542)

AUTHOR (AU): Holden,M.T.; Titball,R.W.; Peacock,S.J.;
Cerdeno-Tarraga,A.M.; Atkins,T.; Crossman,L.C.;
Pitt,T.; Churcher,C.; Mungall,K.; Bentley,S.D.;
Sebahia,M.; Thomson,N.R.; Bason,N.; Beacham,I.R.;
Brooks,K.; Brown,K.A.; Brown,N.F.; Challis,G.L.;

Cherevach,I.; Chillingworth,T.; Cronin,A.; Crossett,B.;
 Davis,P.; DeShazer,D.; Feltwell,T.; Fraser,A.;
 Hance,Z.; Hauser,H.; Holroyd,S.; Jagels,K.; Keith,K.E.;
 Maddison,M.; Moule,S.; Price,C.; Quail,M.A.;
 Rabbinoiwitsch,E.; Rutherford,K.; Sanders,M.;
 Simmonds,M.; Songsivilai,S.; Stevens,K.; Tumapa,S.;
 Vesaratchavest,M.; Whitehead,S.; Yeats,C.;
 Barrell,B.G.; Oyston,P.C.; Parkhill,J.

TITLE (TI): Genomic plasticity of the causative agent of
 melioidosis, *Burkholderia pseudomallei*
 JOURNAL (SO): Proc. Natl. Acad. Sci. U.S.A., 101 (39), 14240-14245
 (2004)
 OTHER SOURCE (OS): CA 141:289864
 REFERENCE: 2 (bases 1 to 4074542)
 AUTHOR (AU): Holden,M.T.G.
 TITLE (TI): Direct Submission
 JOURNAL (SO): Submitted (01-SEP-2004) Submitted on behalf of the
 Pathogen Sequencing Unit, Sanger Institute, Wellcome
 Trust Genome Campus, Hinxton, Cambridge CB10 1SA,
 E-mail: mh3@sanger.ac.uk

FEATURES (FEAT):

| Feature Key | Location | Qualifier |
|-------------|------------|--|
| source | 1..4074542 | /organism="Burkholderia pseudomallei K96243" /mol-type="genomic DNA" /strain="K96243" /db-xref="taxon:272560" /chromosome="1" |

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LOCUS (LOC): BX936398 GenBank (R)
 GenBank ACC. NO. (GBN): BX936398
 GenBank VERSION (VER): BX936398.1 GI:51587641
 CAS REGISTRY NO. (RN): 736028-02-7
 SEQUENCE LENGTH (SQL): 4744671
 MOLECULE TYPE (CI): DNA; circular
 DIVISION CODE (CI): Bacteria
 DATE (DATE): 17 Apr 2005
 DEFINITION (DEF): *Yersinia pseudotuberculosis* IP32953 genome, complete
 sequence.
 KEYWORDS (ST): complete genome
 SOURCE: *Yersinia pseudotuberculosis* IP 32953
 ORGANISM (ORGN): *Yersinia pseudotuberculosis* IP 32953
 Bacteria; Proteobacteria; Gammaproteobacteria;
 Enterobacteriales; Enterobacteriaceae; *Yersinia*
 REFERENCE: 1 (bases 1 to 4744671)
 AUTHOR (AU): Chain,P.S.; Carniel,E.; Larimer,F.W.; Lamerdin,J.;
 Stoutland,P.O.; Regala,W.M.; Georgescu,A.M.;
 Vergez,L.M.; Land,M.L.; Motin,V.L.; Brubaker,R.R.;
 Fowler,J.; Hinnebusch,J.; Marceau,M.; Medigue,C.;
 Simonet,M.; Chenal-Francisque,V.; Souza,B.; Dacheux,D.;
 Elliott,J.M.; Derbise,A.; Hauser,L.J.; Garcia,E.
 TITLE (TI): Insights into the evolution of *Yersinia pestis* through
 whole-genome comparison with *Yersinia*
pseudotuberculosis
 JOURNAL (SO): Proc. Natl. Acad. Sci. U.S.A., 101 (38), 13826-13831
 (2004)
 OTHER SOURCE (OS): CA 141:272420
 REFERENCE: 2 (bases 1 to 4744671)
 AUTHOR (AU): Chain,P.S.G.; Carniel,E.; Garcia,E.; Larimer,F.W.
 TITLE (TI): Direct Submission

CDS

185511..186149

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/gene="eda"  
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aldolase, len: 212aa; similar to  
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eda, 2-keto-4-hydroxyglutarate  
aldolase from Escherichia coli  
(213 aa) fasta scores; E(): 0,  
55.7% identity in 203 aa overlap.  
Contains Pfam match to entry  
PF01081 Aldolase, KDPG and KHG  
aldolase; Prosite match to PS00159  
KDPG and KHG aldolases active site  
and Prosite match to PS00160 KDPG  
and KHG aldolases Schiff-base  
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=> d his full

(FILE 'HOME' ENTERED AT 17:33:10 ON 11 APR 2007)

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AQUASCI, BIOENG, BIOSIS, BIOTECHABS, BIOTECHDS, BIOTECHNO, CABA, CAPLUS,
CEABA-VTB, CIN, CONFSCI, CROPB, CROPU, DDFB, DDFU, DGENE, DISSABS, DRUGB,
DRUGMONOG2, DRUGU, EMBAL, EMBASE, ...' ENTERED AT 17:33:40 ON 11 APR 2007
SEA RESTRICTI? (S) (ENZYM? OR ENDONUCLEAS?)

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10  FILE ADISINSIGHT  
27  FILE ADISNEWS  
3911 FILE AGRICOLA  
116  FILE ANABSTR  
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41  FILE AQUALINE  
1216 FILE AQUASCI  
3267 FILE BIOENG  
30282 FILE BIOSIS  
10641 FILE BIOTECHABS  
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10704 FILE CABA  
37645 FILE CAPLUS  
790  FILE CEABA-VTB  
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4  FILE CROPB  
133  FILE CROPU  
29  FILE DDFB  
170  FILE DDFU  
38469 FILE DGENE  
2384  FILE DISSABS  
29  FILE DRUGB  
566  FILE DRUGU  
125  FILE EMBAL  
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10560 FILE ESBIODASE  
16  FILE FOREGE  
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1211 FILE FSTA  
515097 FILE GENBANK  
61  FILE HEALSAFE  
6488 FILE IFIPAT
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 25 FILE KOSMET
 17980 FILE LIFESCI
 39232 FILE MEDLINE
 240 FILE NTIS
 1 FILE NUTRACEUT
 371 FILE OCEAN
 13245 FILE PASCAL
 1 FILE PHAR
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 745 FILE PROMT
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 19895 FILE SCISEARCH
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 65679 FILE USPATFULL
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 1 FILE VETB
 161 FILE VETU
 68 FILE WATER
 8559 FILE WPIDS
 31 FILE WPIFV
 8559 FILE WPINDEX
 42 FILE IPA
 4 FILE NAPRALERT
 555 FILE NLDB

L1 QUE RESTRICTI? (S) (ENZYM? OR ENDONUCLEAS?)

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FILE 'GENBANK, USPATFULL, MEDLINE, CAPLUS, BIOSIS, EMBASE, SCISEARCH,
 BIOTECHNO, LIFESCI, PASCAL, CABA' ENTERED AT 17:37:30 ON 11 APR 2007

L2 790629 SEA RESTRICTI? (S) (ENZYM? OR ENDONUCLEAS?)
 L3 739 SEA L2(S) PYLORI?
 L4 49 SEA L3 AND (BCC? OR ?CCATC?)
 L5 47 DUP REM L4 (2 DUPLICATES REMOVED)
 D TI L5 1-45
 D TI L5 46-47
 L6 31 SEA L3 AND (BCC? OR CCATC?)
 L7 29 DUP REM L6 (2 DUPLICATES REMOVED)
 D L7 1-29

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FILE GENBANK

GENBANK (R) IS A REGISTERED TRADEMARK OF THE U.S. DEPARTMENT
 OF HEALTH AND HUMAN SERVICES.

This file contains CAS Registry Numbers for easy and accurate
 substance identification.

FILE USPATFULL

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